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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/887,052

DATE: 07/07/2001  
TIME: 12:54:39

Input Set : A:\204212US0X.txt  
Output Set: N:\CRF3\07062001\I887052.raw

3 <110> APPLICANT: MOECKEL, Bettina  
 4 BATHE, Brigitte  
 5 HERMANN, Thomas  
 6 PFEFFERLE, Walter  
 7 BINDER, Michael  
 9 <120> TITLE OF INVENTION: NUCLEOTIDE SEEQUENCES WHICH CODE FOR THE rpoB GENE  
 11 <130> FILE REFERENCE: 204212US0X  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/887,052  
 C--> 13 <141> CURRENT FILING DATE: 2001-06-25  
 13 <150> PRIOR APPLICATION NUMBER: DE10107229.5  
 14 <151> PRIOR FILING DATE: 2001-02-16  
 16 <160> NUMBER OF SEQ ID NOS: 8  
 18 <170> SOFTWARE: PatentIn version 3.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 5099  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Corynebacterium glutamicum  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (702)..(4196)  
 29 <400> SEQUENCE: 1  
 30 acaatgtgac tcgtgatttt tgggtggatc agcgtaccgg tttgggttgc gatctagctg 60  
 32 aaaatattga tgattttac ggcgaccgca gcggccagaa gtacgaacag aaattgctt 120  
 34 tcgacgcctc cctcgacgat gcagctgtct ctaagctggt tgcacaggcc gaaagcatcc 180  
 36 ctgatggaga tgtgagcaaa atcgc当地ata ccgttaggtat tgtgatcggt gcggatttgg 240  
 38 ctctcggtgg cctggccggg tttttgggg cgtttggaa gaaacgtcga gaagcttaac 300  
 40 ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tgtttgctag 360  
 42 ggtgcctcgt agaagggtc aagaagattt ctggaaacg cggccgtcgt gttgggtgct 420  
 44 aatagcacgc ggagcaccag atgaaaaatc tccctttac ttccgcgcgc gattggata 480  
 46 ctctgagtcg ttgcgttgg attcgtgact cttttcggtt cctgttagcgc caagacattt 540  
 48 atcaagggtgg tttaaaaaaa ccgatttgcac aaggtcattc agtgc当地atct ggagtgcgttc 600  
 50 agggggatcg gttccctcag cagaccaatt gtc当地aaat accagcgggtt ttgatctgca 660  
 52 cttaatggcc ttgaccagcc aggtgc当地attt accccgcgtga g gtg ctg gaa gga ccc 716  
 53 Val Leu Glu Gly Pro  
 54 1 5  
 56 atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt 764  
 57 Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly  
 58 10 15 20  
 60 gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg 812  
 61 Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val  
 62 25 30 35  
 64 ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt 860  
 65 Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly  
 66 40 45 50  
 68 acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc 908  
 69 Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala  
 70 55 60 65

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72	cgc	gta	acc	agc	ggc	ctt	gag	aac	att	ctc	gag	gag	ctc	tcc	cca	atc	956
73	Arg	Val	Thr	Ser	Gly	Leu	Glu	Asn	Ile	Leu	Glu	Glu	Leu	Ser	Pro	Ile	
74	70					75				80						85	
76	cag	gat	tac	tct	gga	aac	atg	tcc	ctg	agc	ctt	tcg	gag	cca	cgc	ttc	1004
77	Gln	Asp	Tyr	Ser	Gly	Asn	Met	Ser	Leu	Ser	Leu	Ser	Glu	Pro	Arg	Phe	
78						90				95						100	
80	gaa	gac	gtc	aag	aac	acc	att	gac	gag	gcg	aaa	gaa	aag	gac	atc	aac	1052
81	Glu	Asp	Val	Lys	Asn	Thr	Ile	Asp	Glu	Ala	Lys	Glu	Lys	Asp	Ile	Asn	
82						105				110						115	
84	tac	gcg	gcg	cca	ctg	tat	gtg	acc	gcg	gag	ttc	gtc	aac	acc	acc		1100
85	Tyr	Ala	Ala	Pro	Leu	Tyr	Val	Thr	Ala	Glu	Phe	Val	Asn	Asn	Thr	Thr	
86						120				125						130	
88	ggt	gaa	atc	aag	tct	cag	act	gtc	ttc	atc	ggc	gat	ttc	cca	atg	atg	1148
89	Gly	Glu	Ile	Lys	Ser	Gln	Thr	Val	Phe	Ile	Gly	Asp	Phe	Pro	Met	Met	
90						135				140						145	
92	acg	gac	aag	gga	acg	ttc	atc	atc	aac	gga	acc	gaa	cgc	gtt	gtg	gtc	1196
93	Thr	Asp	Lys	Gly	Thr	Phe	Ile	Ile	Asn	Gly	Thr	Glu	Arg	Val	Val	Val	
94						150				155						165	
96	agc	cag	ctc	gtc	cgc	tcc	ccg	ggc	gtg	tac	ttt	gac	cag	acc	atc	gat	1244
97	Ser	Gln	Leu	Val	Arg	Ser	Pro	Gly	Val	Tyr	Phe	Asp	Gln	Thr	Ile	Asp	
98						170				175						180	
100	aag	tca	act	gag	cgt	cca	ctg	cac	gcc	gtg	aag	gtt	att	cct	tcc	cgt	1292
101	Lys	Ser	Thr	Glu	Arg	Pro	Leu	His	Ala	Val	Lys	Val	Ile	Pro	Ser	Arg	
102						185				190						195	
104	ggt	gct	tgg	ctt	gag	ttt	gac	gtc	gat	aag	cgc	gat	tcg	gtt	ggt	gtt	1340
105	Gly	Ala	Trp	Leu	Glu	Phe	Asp	Val	Asp	Lys	Arg	Asp	Ser	Val	Gly	Val	
106						200				205						210	
108	cgt	att	gac	cgc	aag	cgt	cgc	cag	cca	gtc	acc	gta	ctg	ctg	aag	gct	1388
109	Arg	Ile	Asp	Arg	Lys	Arg	Arg	Gln	Pro	Val	Thr	Val	Leu	Leu	Lys	Ala	
110						215				220						225	
112	ctt	ggc	tgg	acc	act	gag	cag	atc	acc	gag	cgt	ttc	ggt	ttc	tct	gaa	1436
113	Leu	Gly	Trp	Thr	Glu	Gln	Ile	Thr	Glu	Arg	Phe	Gly	Phe	Ser	Glu		
114						230				235						245	
116	atc	atg	atg	tcc	acc	ctc	gag	tcc	gat	ggt	gta	gca	acc	acc	gat	gag	1484
117	Ile	Met	Met	Ser	Thr	Leu	Glu	Ser	Asp	Gly	Val	Ala	Asn	Thr	Asp	Glu	
118						250				255						260	
120	gca	ttg	ctg	gag	atc	tac	cgc	aag	cag	cgt	cca	ggc	gag	cag	cct	acc	1532
121	Ala	Leu	Leu	Glu	Ile	Tyr	Arg	Lys	Gln	Arg	Pro	Gly	Glu	Gln	Pro	Thr	
122						265				270						275	
124	cgc	gac	ctt	gcg	cag	tcc	ctc	ctg	gac	aac	agc	ttc	ttc	cgt	gca	aag	1580
125	Arg	Asp	Leu	Ala	Gln	Ser	Leu	Leu	Asp	Asn	Ser	Phe	Phe	Arg	Ala	Lys	
126						280				285						290	
128	cgc	tac	gac	ctg	gct	cgc	gtt	ggt	cgt	tac	aag	atc	aac	cgc	aag	ctc	1628
129	Arg	Tyr	Asp	Leu	Ala	Arg	Val	Gly	Arg	Tyr	Lys	Ile	Asn	Arg	Lys	Leu	
130						295				300						305	
132	ggc	ctt	ggt	ggc	gac	cac	gat	ggt	ttg	atg	act	ctt	act	gaa	gag	gac	1676
133	Gly	Leu	Gly	Gly	Asp	His	Asp	Gly	Leu	Met	Thr	Leu	Thr	Glu	Glu	Asp	
134						310				315						320	325
136	atc	gca	acc	acc	atc	gag	tac	ctg	gtg	cgt	ctg	cac	gca	ggt	gag	cgc	1724

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137	Ile	Ala	Thr	Thr	Ile	Glu	Tyr	Leu	Val	Arg	Leu	His	Ala	Gly	Glu	Arg	
138					330				335					340			
140	gtc	atg	act	tct	cca	aat	ggt	gaa	gag	atc	cca	gtc	gag	acc	gat	gac	1772
141	Val	Met	Thr	Ser	Pro	Asn	Gly	Glu	Glu	Ile	Pro	Val	Glu	Thr	Asp	Asp	
142					345				350					355			
144	atc	gac	cac	ttt	ggt	aac	cgt	cgt	ctg	cgt	acc	gtt	ggc	gaa	ctg	atc	1820
145	Ile	Asp	His	Phe	Gly	Asn	Arg	Arg	Leu	Arg	Thr	Val	Gly	Glu	Leu	Ile	
146					360				365					370			
148	cag	aac	cag	gtc	cgt	gtc	ggc	ctg	tcc	cgc	atg	gag	cgc	gtt	gtt	cgt	1868
149	Gln	Asn	Gln	Val	Arg	Val	Gly	Leu	Ser	Arg	Met	Glu	Arg	Val	Val	Arg	
150					375				380					385			
152	gag	cgt	atg	acc	acc	cag	gat	gcg	gag	tcc	att	act	cct	act	tcc	ttg	1916
153	Glu	Arg	Met	Thr	Thr	Gln	Asp	Ala	Glu	Ser	Ile	Thr	Pro	Thr	Ser	Leu	
154	390				395				400					405			
156	atc	aac	gtt	cgt	cct	gtc	tct	gca	gct	atc	cgt	gag	ttc	ttc	gga	act	1964
157	Ile	Asn	Val	Arg	Pro	Val	Ser	Ala	Ala	Ile	Arg	Glu	Phe	Phe	Gly	Thr	
158					410				415					420			
160	tcc	cag	ctg	tct	cag	ttc	atg	gac	cag	aac	acc	tcc	ctg	tct	ggt	ttg	2012
161	Ser	Gln	Leu	Ser	Gln	Phe	Met	Asp	Gln	Asn	Asn	Ser	Leu	Ser	Gly	Leu	
162					425				430					435			
164	act	cac	aag	cgt	cgt	ctg	gct	ctg	ggc	ccg	ggg	ggg	gtt	ctg	tcc	cgt	2060
165	Thr	His	Lys	Arg	Arg	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Gly	Leu	Ser	Arg	
166					440				445					450			
168	gag	cgc	gcc	ggc	atc	gag	gtt	cga	gac	gtt	cac	cca	tct	cac	tac	ggc	2108
169	Glu	Arg	Ala	Gly	Ile	Glu	Val	Arg	Asp	Val	His	Pro	Ser	His	Tyr	Gly	
170					455				460					465			
172	cgt	atg	tgc	cca	att	gag	act	ccg	gaa	ggt	cca	aac	att	ggc	ctg	atc	2156
173	Arg	Met	Cys	Pro	Ile	Glu	Thr	Pro	Glu	Gly	Pro	Asn	Ile	Gly	Leu	Ile	
174	470				475				480					485			
176	ggt	tcc	ttg	gct	tcc	tat	gct	cga	gtg	aac	cca	ttc	ggt	ttc	att	gag	2204
177	Gly	Ser	Leu	Ala	Ser	Tyr	Ala	Arg	Val	Asn	Pro	Phe	Gly	Phe	Ile	Glu	
178					490				495					500			
180	acc	cca	tac	cgt	cgc	atc	atc	gac	ggc	aag	ctg	acc	gac	cag	att	gac	2252
181	Thr	Pro	Tyr	Arg	Arg	Ile	Ile	Asp	Gly	Lys	Leu	Thr	Asp	Gln	Ile	Asp	
182					505				510					515			
184	tac	ctt	acc	gct	gat	gag	gaa	gac	cgc	ttc	gtt	gct	ggc	cag	gca	aac	2300
185	Tyr	Leu	Thr	Ala	Asp	Glu	Glu	Asp	Arg	Phe	Val	Val	Ala	Gln	Ala	Asn	
186					520				525					530			
188	acg	cac	tac	gac	gaa	gag	ggc	aac	atc	acc	gat	gag	acc	gtc	act	gtt	2348
189	Thr	His	Tyr	Asp	Glu	Glu	Gly	Asn	Ile	Thr	Asp	Glu	Thr	Val	Thr	Val	
190					535				540					545			
192	cgt	ctg	aag	gac	ggc	gac	atc	gcc	atg	gtt	ggc	cgc	aac	gct	gtt	gat	2396
193	Arg	Leu	Lys	Asp	Gly	Asp	Ile	Ala	Met	Val	Gly	Arg	Asn	Ala	Val	Asp	
194					550				555					560		565	
196	tac	atg	gac	gtt	tcc	cct	cgt	cag	atg	gtt	tct	ggt	acc	gct	atg		2444
197	Tyr	Met	Asp	Val	Ser	Pro	Arg	Gln	Met	Val	Ser	Val	Gly	Thr	Ala	Met	
198					570				575					580			
200	att	cca	ttc	ctg	gag	cac	gac	gat	gct	aac	cgt	gca	ctg	atg	ggc	gct	2492
201	Ile	Pro	Phe	Leu	Glu	His	Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Ala	

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202	585	590	595	
204	aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc			2540
205	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe			
206	600	605	610	
208	gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg			2588
209	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu			
210	615	620	625	
212	gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc			2636
213	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe			
214	630	635	640	645
216	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt			2684
217	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg			
218	650	655	660	
220	aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg			2732
221	Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu			
222	665	670	675	
224	gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt			2780
225	Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly			
226	680	685	690	
228	cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt			2828
229	Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val			
230	695	700	705	
232	gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc			2876
233	Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu			
234	710	715	720	725
236	aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag			2924
237	Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu			
238	730	735	740	
240	gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc			2972
241	Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile			
242	745	750	755	
244	acc cgc gac atc cct aat gtt tct gaa gaa gtc ctc aag gac ctc gac			3020
245	Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp			
246	760	765	770	
248	gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc			3068
249	Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile			
250	775	780	785	
252	ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa			3116
253	Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu			
254	790	795	800	805
256	gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc			3164
257	Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg			
258	810	815	820	
260	gat acc tcc atg aag gtt cct cac ggt gag acc ggc aag gtc atc ggc			3212
261	Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly			
262	825	830	835	
264	gtg cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc			3260
265	Val Arg. His Phe Ser Arg Glu Asp Asp Asp Asp Leu Ala Pro Gly Val			
266	840	845	850	

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268 aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac	3308
269 Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp	
270 855 860 865	
272 ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa	3356
273 Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys	
274 870 875 880 885	
276 att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt	3404
277 Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val	
278 890 895 900	
280 gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt	3452
281 Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly	
282 905 910 915	
284 cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc	3500
285 Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser	
286 920 925 930	
288 gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct	3548
289 Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro	
290 935 940 945	
292 gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg	3596
293 Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val	
294 950 955 960 965	
296 ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca	3644
297 Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser	
298 970 975 980	
300 cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca	3692
301 Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala	
302 985 990 995	
304 acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737
305 Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val	
306 1000 1005 1010	
308 tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782
309 Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp	
310 1015 1020 1025	
312 gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc	3827
313 Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr	
314 1030 1035 1040	
316 cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc	3872
317 Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe	
318 1045 1050 1055	
320 ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac	3917
321 Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr	
322 1060 1065 1070	
324 aca ctt cag gag ctg ctg acc atc aag tct gat gac gtc gtt ggc	3962
325 Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly	
326 1075 1080 1085	
328 cgt gtc aag gtc tac gaa gca att gtc aag ggc gag aac atc ccg	4007
329 Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro	
330 1090 1095 1100	
332 gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date